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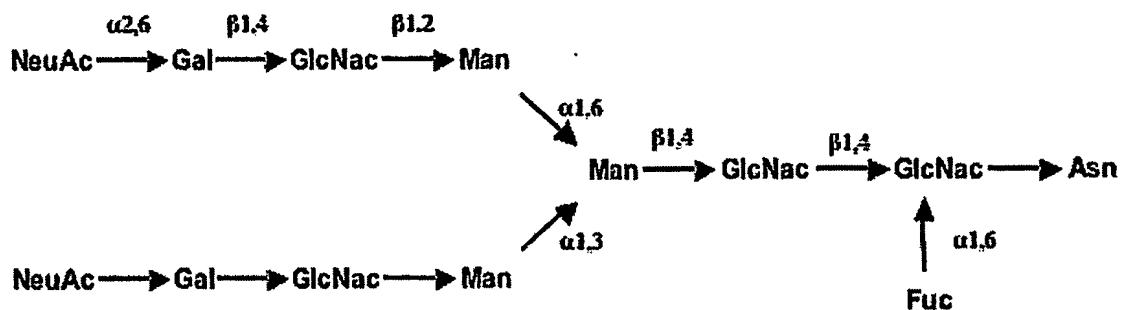


Figure 1

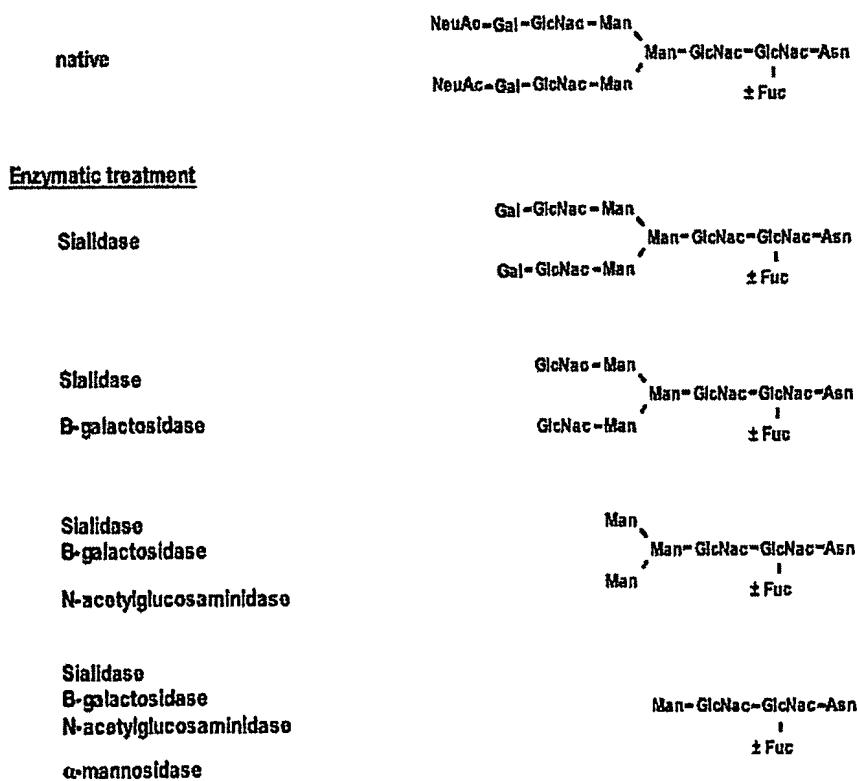
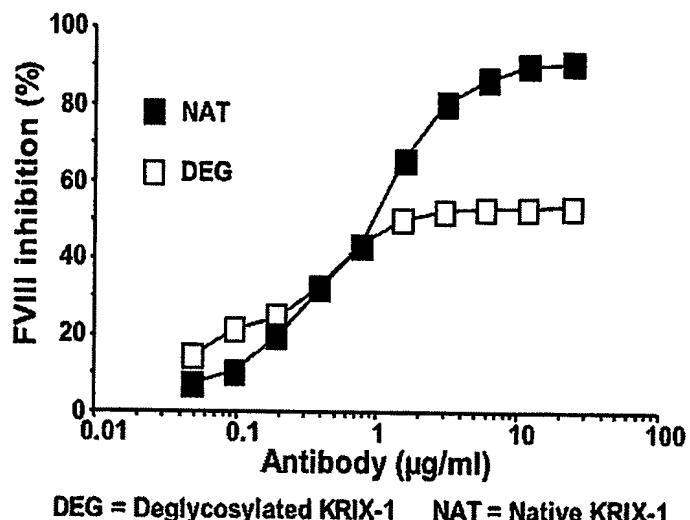
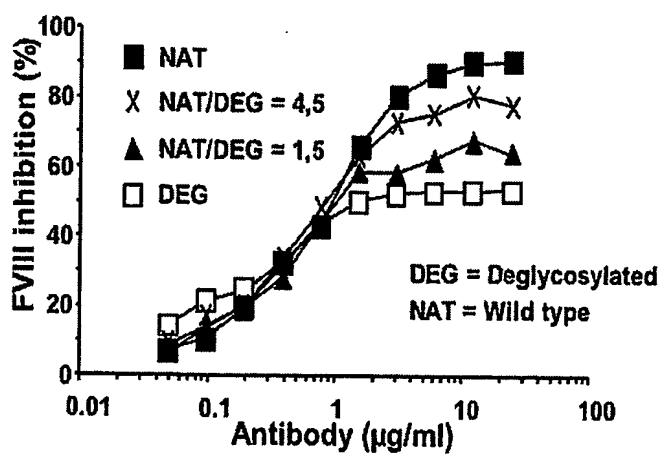
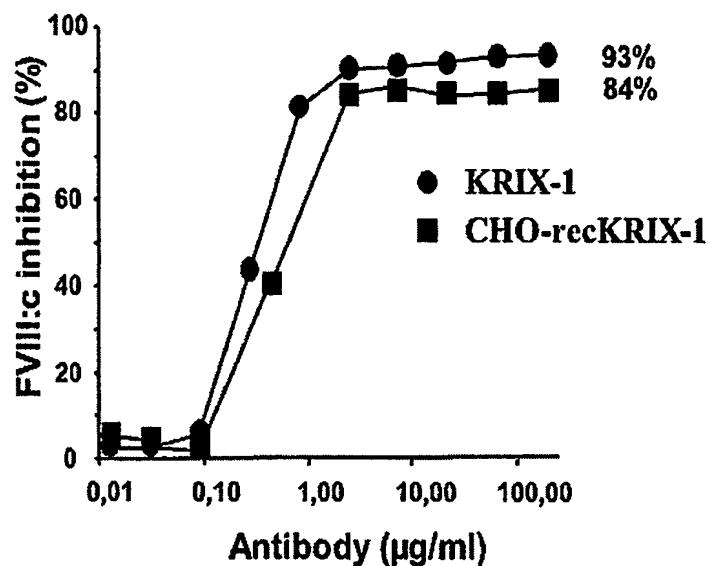
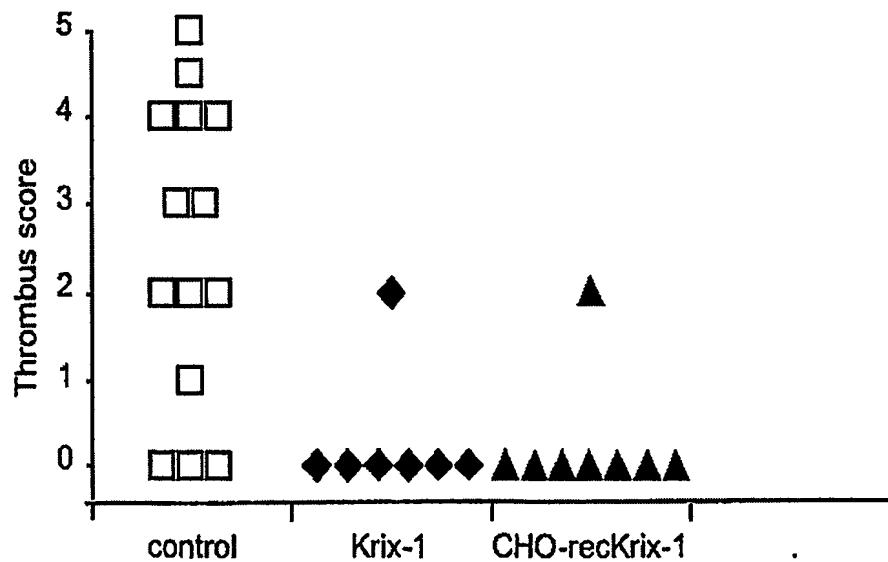
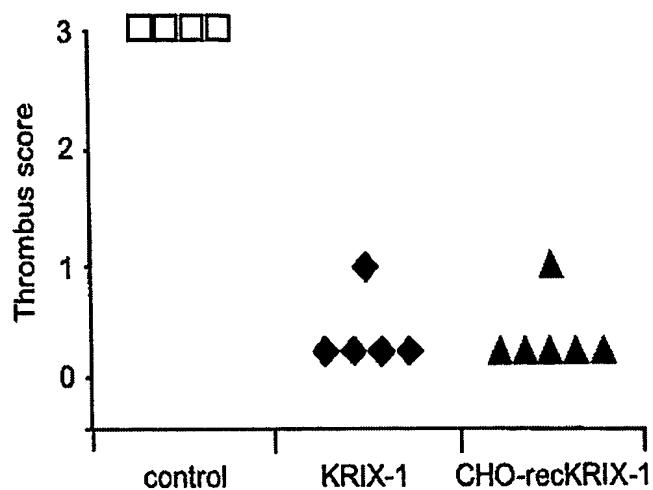
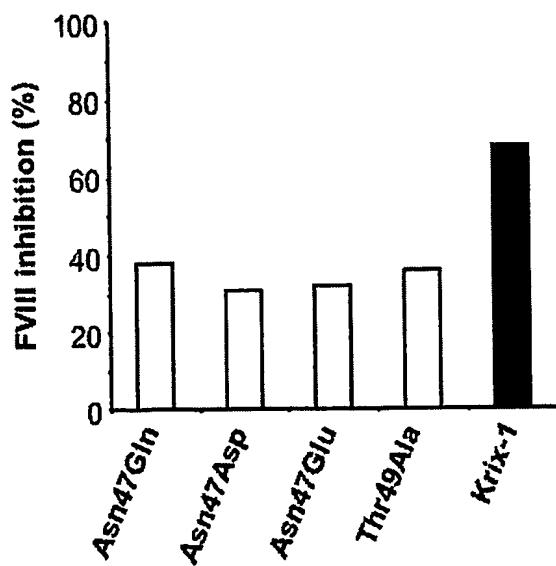


Figure 2

2/14**Figure 3****Figure 4**

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**Figure 5****Figure 6**

4/14**Figure 7****Figure 8**

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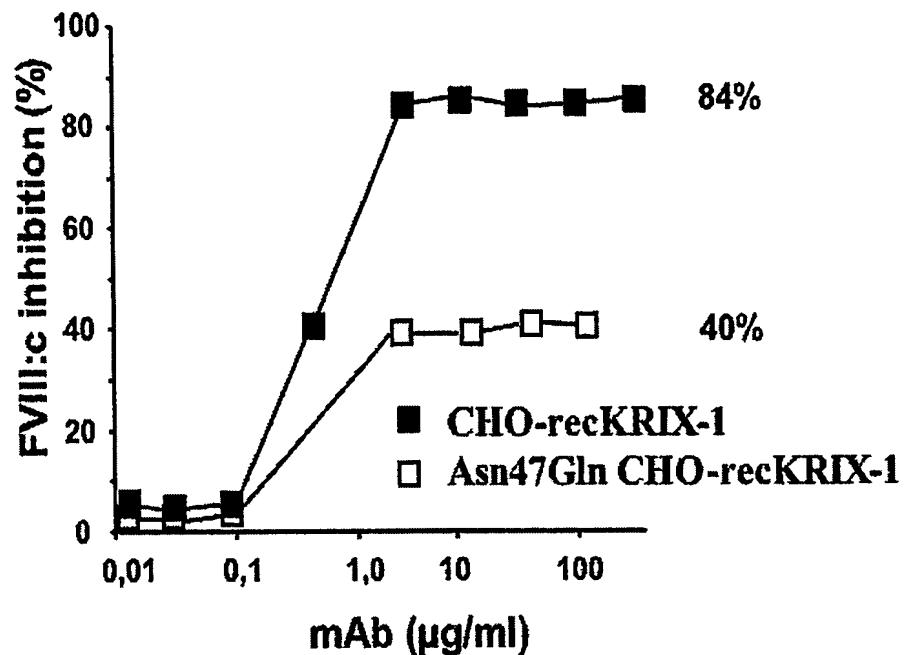


Figure 9

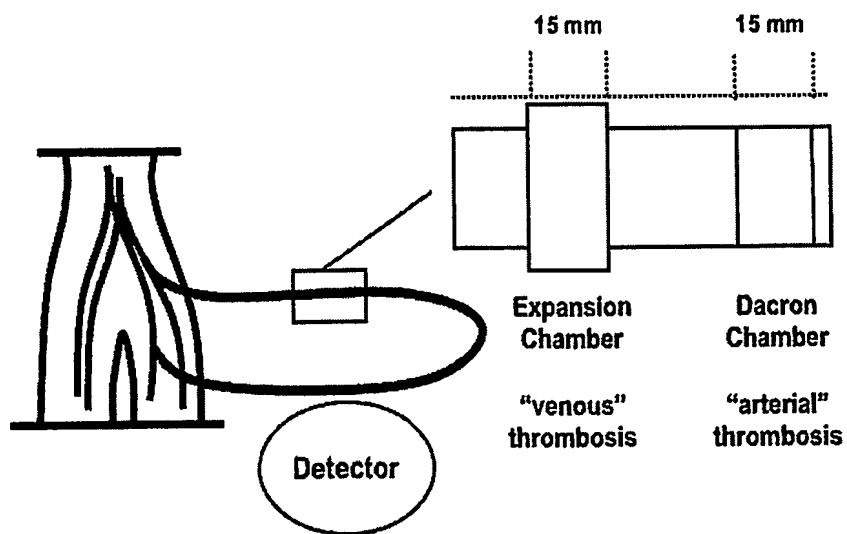
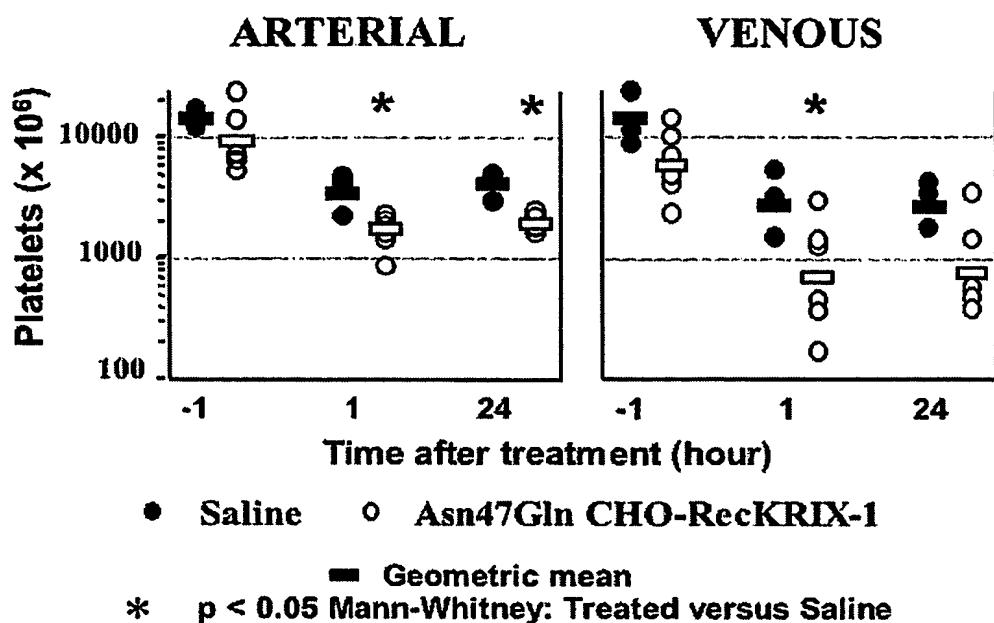
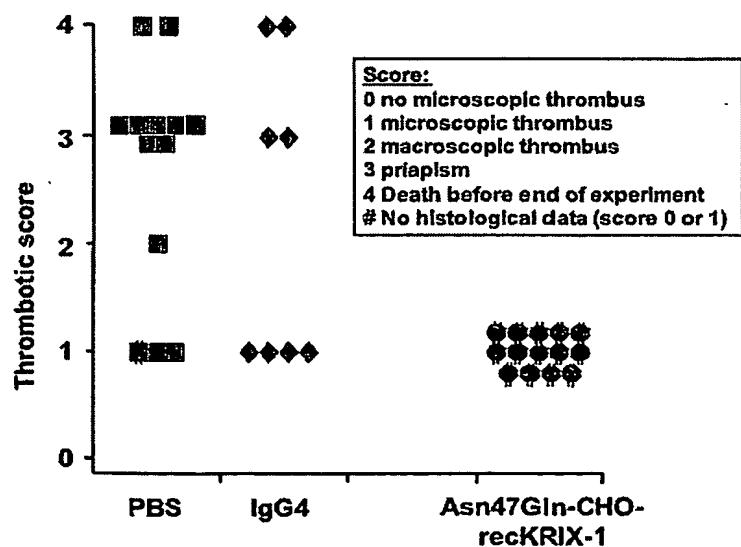
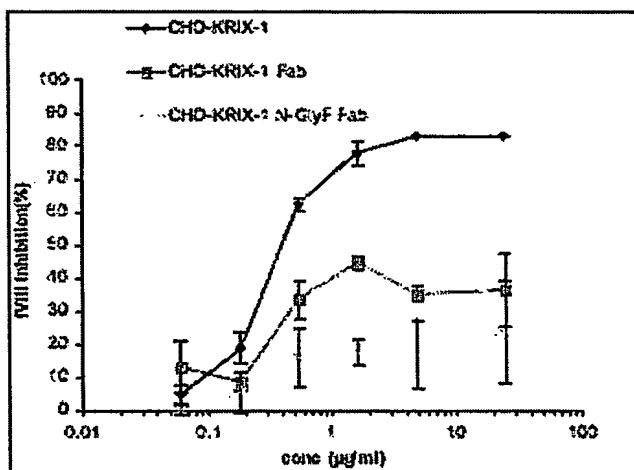
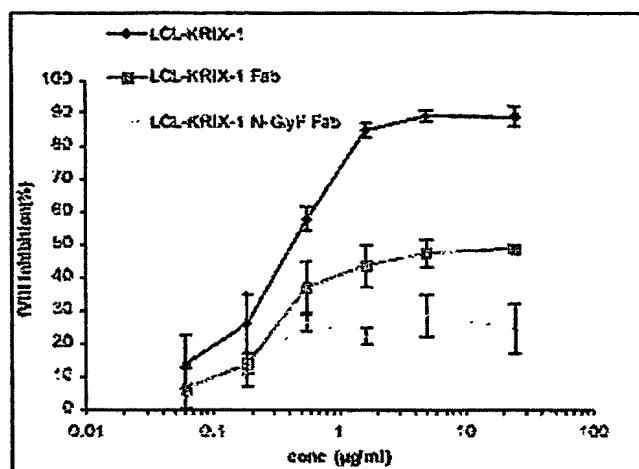
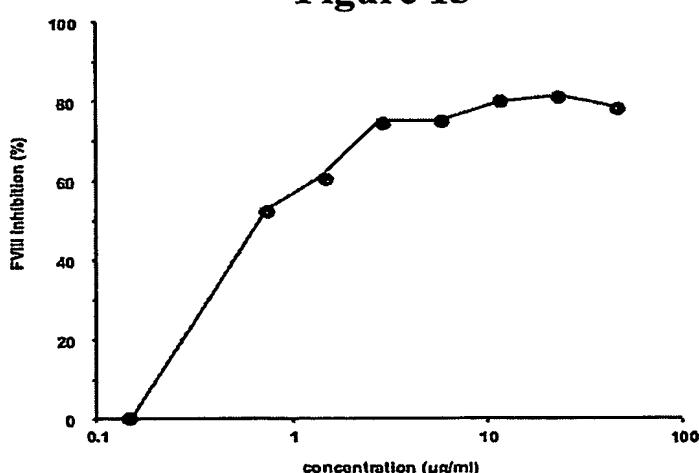


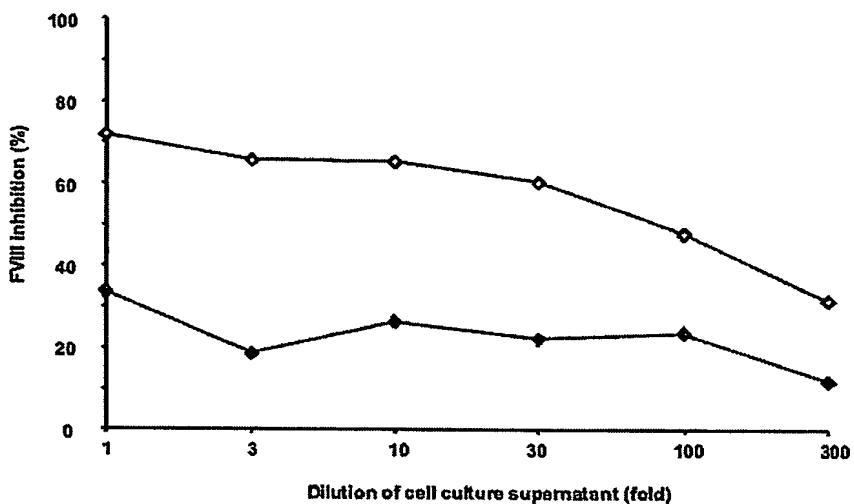
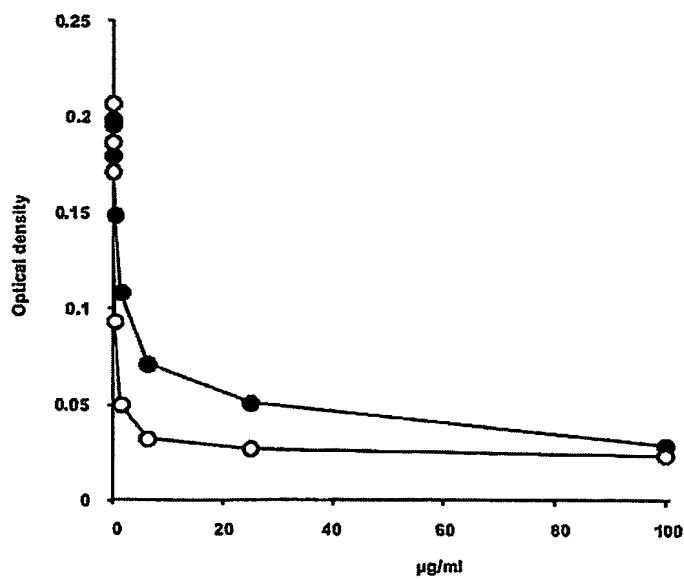
Figure 10

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**Figure 11****Figure 12**

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**Figure 13****Figure 14**

8/14**Figure 15****Figure 16**

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Krix-1 Variable heavy chain (SEQ ID NO: 1 and 2)

1/1 31/11
 ATG GAC TGG ACC TGG AGG ATC CTC TTC TTG GTG GCA GCA GCC ACA GGA GCC CAC TCC CAG
 M D W T W R I L F L V A A A T G A H S Q
 <----- Leader peptide ----->

 61/21 91/31
 GTG CAA CTG GTG CAA TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTC TCC
 V Q L V Q S G A E V K K P G A S V K V S

 121/41 47 49 151/51
 TGC AAG ACC TCT GGA TAC AAC TTC ACC GGC TAC TCT GCT TCT GGA CAT ATC TTC ACC GCC
 C K T S G Y N F T G Y S A S G H I F T A
 * *
 <----- CDR1 ----->

 181/61 211/71
 TAC TCT GTG CAC TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA AGG ATC
 Y S V H W V R Q A P G Q G L E W M G R I
 ----->
 <-----

 241/81 271/91
 AAC CCT AAC AGT GGT GCC ACA GAC TAT GCA CAT AAA TTT CAG GGC AGG GTC ACC ATG TCC
 N P N S G A T D Y A H K F Q G R V T M S
 ----->
 CDR2

 301/101 331/111
 AGG GAC ACG TCC ATC AGC ACA GCC TAC ATG GAA CTG AGC AGG CTG ACA TCT GAC GAC ACG
 R D T S I S T A Y M E L S R L T S D D T

 361/121 391/131
 GCC ATG TAT TAC TGT GCG AGA GCC GAC AAC TAT TTC GAT ATT GTG ACT GGC TAT ACT TCT
 A M Y Y C A R A D N Y F D I V T G Y T S
 <----- CDR3 ----->

 421/141 451/151
 CAT TAC TTT GAC TAC TGG GGC CGG GGA ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG
 H Y F D Y W G R G T L V T V S S A S T K
 ----->

 481/161
 GGC CCA TCG GTC TTC C
 G P S V F

Figure 17

10/14

Krix-1 Variable light chain (SEQ ID NO: 3 and 4)

1/1 31/11
 ATG GAA ACC CCA GCT CAG CTT CTC TTC CTC CTG CTA CTC TGG CTC CCA GAT ACC ACC GGA
 M E T P A Q L L F L L L W L P D T T G
 <----- Leader ----->

61/21 91/31
 GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC
 E I V L T Q S P G T L S L S P G E R A T

121/41 151/51
 CTC TCC TGC AGG GCC AGT CAG AGT GTT GCC AGC GCC TAC TTA GCC TGG TAC CAG CAA AAA
 L S C R A S Q S V A S A Y L A W Y Q Q K
 <----- CDR1 ----->

181/61 211/71
 CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT GCA TCC AGT AGG GCC ACC GAC ATC CCA
 P G Q A P R L L I Y G A S S R A T D I P
 <----- CDR2 ----->

241/81 271/91
 CAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG
 H R F S G S G S G T D F T L T I S R L E

301/101 331/111
 CCT GAA GAT TTT GCA GTG TAC TAC TGT CAG CAA TAT GGT ACC TCA GCC TTA CTC ACT TTC
 P E D F A V Y Y C Q Q Y G T S A L L T F
 <----- CDR3 ----->

361/121 391/131
 GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC
 G G G T K V E I K R T V A A P S V F I F

421/141
 CCG CCA TCT
 P P S

Figure 17 (continued)

11/14

scFvLE2E9VLVH Q(His) (SEQ ID 25 and 26)

1/1 31/11
 atg gaa acc cca gcg cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca gat acc acc acc gga
 M E T P A Q L L F L L L W L P D T T G
 <----- Leader peptide ----->

61/21 91/31
gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc acc
E I V L T Q S P G T L S L S P G E R A T
<-----

121/41 151/51
ctc tcc tgc agg gcc agt cag agt gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa
L S C R A S Q S V A S A Y L A W Y Q Q K

181/61 211/71
cct ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca
P G Q A P R L L I Y G A S S R A T D I P
----- VLJk -----

241/81	271/91
cac agg ttc agt ggc agt ggg tat ggg aca gac ttc act ctc acc atc agc aga ctg gag	H R F S G S G S G T D F T L T I S R L E

301/101 331/111
 cct gaa gat ttt gca gtg tac tac tgt cag caa tat ggt acc tca gcc tta ctc act ttc
 P E D F A V Y Y C Q Q Y G T S A L L T F

361/121 391/131
 ggc gga ggg acc aag gtg gag atc aaa cga ggt gga ggc ggt tca ggc gga ggt ggc tct
 G G G T K V E I K R G G G G S G G G G S
 -----> <----- Linker ---

421/141 451/151
 ggc ggt ggc gga tcg cag gta cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg
 G G G G S Q V Q L V Q S G A E V K K P G
 -----> <-----

481/161	511/171
gcc tca gtg aag gtc tcc tgc aag acc tct	gga tac caa ttc acc ggc tac tct gct tct
A S V K V S C K T S	G Y Q F T G Y S A S

541/181	571/191
gga cat atc ttc acc gcc tac tct gtg cac	tgg gtg cga cag gcc cct gga caa ggg ctt
G H I F T A Y S V H	W V R Q A P G Q G L

Figure 18

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601/201

gag tgg atg gga agg atc aac cct aac agt ggt gcc aca gac tat gca cat aaa ttt cag
E W M G R I N P N S G A T D Y A H K F Q
----- VHDJH -----

661/221

ggc agg gtc acc atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg agc agg
G R V T M S R D T S I S T A Y M E L S R

721/241

ctg aca tct gac gac aca gcc atg tat tac tgt gcg aga gcc gac aac tat ttc gat att
L T S D D T A M Y Y C A R A D N Y F D I

781/261

gtg act ggc tat act tct cat tac ttt gac tac tgg ggc cgg gga acc ctg gtc acc gtc
V T G Y T S H Y F D Y W G R G T L V T V

841/281

tcc tca cat cat cat cat cat cat tga
S S H H H H H H *
-----> <----- His(6)tag ----->

Figure 18 (continued)

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RHD5 heavy chain variable region (SEQ ID NO: 29 and 30)

1/1 31/11
 ATG GAC TGG ACC TGG AGG TTC CTC TTT GTG GTG GCA GCA GCT GCA GGT GTC CAG TCC CAG
 M D W T W R F L F V V A A A A A G V Q S Q
 <----- Leader peptide ----->
 61/21 91/31
 GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG CCC GGG TCG TCG GTG ATG GTC TCC
 V Q L V Q S G A E V K K P G S S V M V S
 121/41 151/51
 TGC AAG GCT TCT GGA GGC ACC TTC AGC AGC TTT GGT ATC AGC TGG GTG CGA CAG GCC CCT
 C K A S G G T F S S F G I S W V R Q A P
 <----- CDR1 ----->
 181/61 211/71
 GGA CAA GGG CTT GAG TGG GTG GGA GGG ATC ATC CCT ATC TTT GGT ACA GCA AAC ACC GCA
 G Q G L E W V G G I I P I F G T A N T A
 <----- CDR2 ----->
 241/81 271/91
 CGG AAC TTC CAG AAT AGA GTC ACC ATT ACC GCG GAC GAA TTC ACG AGC ACA GCC TAC ATA
 R N F Q N R V T I T A D E F T S T A Y I
 ----->
 301/101 331/111
 CGA CTG AGG AGC CTG AGA TCT GAA GAT ACG GCC GTG TAT TAC TGT GTC GGC GGT CGA GAT
 R L R S L R S E D T A V Y Y C V G G R D
 -----<
 361/121 391/131
 GCC TAC AGC TTT GAT GGT TTT GAT GTC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA
 A Y S F D G F D V W G Q G T M V T V S S
 ----- CDR3 ----->
 421/141
 GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC
 A S T K G P S V F P
 <----- constant region ----->

Figure 19

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RHD5 Light Chain Variable Region (SEQ ID N0: 31 And 32)

1/1 31/11
ATG GCA TGG ATC CCT CTC TTC CTC GGC GTC CTT GTT TAC TGC ACA GGA TCC GTG GCC TCC
M A W I P L F L G V L V Y C T G S V A S
<----- Leader peptide ----->

61/21 91/31
TCT GGG CTG ACT CAG CCA CAC TCA GTG TCC GTG TCC CCA GGA CAG ACA GCC AAC ATC ACC
S G L T Q P H S V S V S P G Q T A N I T

121/41 151/51
TGC TCT AGA GAT AAG TTG GGT CAT AAA TTT GCT TCC TGG TAT CAA CAG AAG CCA GGC CAG
C S R D K L G H K F A S W Y Q Q K P G Q
<----- CDR1 ----->

181/61 211/71
TCC CCT GCT CTT CTC ATC TAT CAA GAC AGC AAG CGG CCC TCA GGG ATC CCT GAG CGA TTC
S P A L L I Y Q D S K R P S G I P E R F
 \leftarrow ----- CDR2 ----->

241/81 271/91
TCT GGC TCC AAC TCT GGG AAC ACA GCC ACT CTG ACC ATC AGC GGG ACC CAG GCT ATG GAT
S G S N S G N T A T L T I S G T Q A M D

301/101 331/111
 GAG GCT GAC TAT TAC TGT CAG GCG TGG GAC AAC ACC ACT GCC GTA TTC GGC GGA GGG ACC
 E A D Y Y C Q A W D N T T A V F G G G G T
 <----- CDR3 ----->
 * * *

361/121 391/131
AAG TTG ACA GTC CTA AGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC
K L T V L S Q P K A A P S V T L F P P S
<----- constant region ----->

Figure 19 (continued)